Phytotaxa

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Discovery of a new species and a new geographical record of *Metarhizium* (Clavicipitaceae, Hypocreales) from China

Yu yang, yuan-poin xiao, kevin d. hyde, ruvishika s. Jayawardena, yong-zhong Lu, Ausana Mapook, Somrudee Nilthong, Fatimah Al-OTIBI, SHU-Qiong Xie, XI Ang-dong li

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Molecular phylogeny and morphology reveal a new wood-inhabiting fungus, *Hyphoderma cinereofuscum* (Polyporales, Basidiomycota), from southwest China

Wen li, xiyan Wang, daxiang chen, size zhang, yunchao li, changelin zhao, zhongyi zhan

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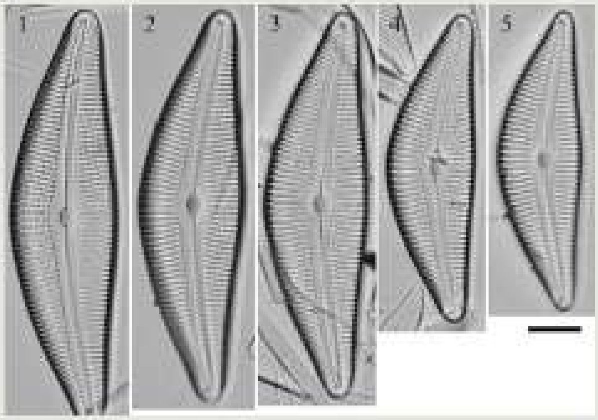

Cymbella erhaiensis sp. nov., a new cymbelloid diatom species (Cymbellales, Bacillariophyta) from Yunnan Province, China*Cymbella erhaiensis sp. nov.*, a new cymbelloid diatom species (Cymbellales, Bacillariophyta) from Yunnan Province, China

KUN ZHENG, QIAO-ZHI XIAO, JI-SHU GUO, JI-MIN HUANG, YUN ZHANG, JOHN PATRICK KOCIOLEK, YAN-LING LI

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Cudonia mongolica sp. nov. (Cudoniaceae, Rhytismatales) from Mongolia

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DUVIER J. ATUESTA, RAFAEL TREVISAN

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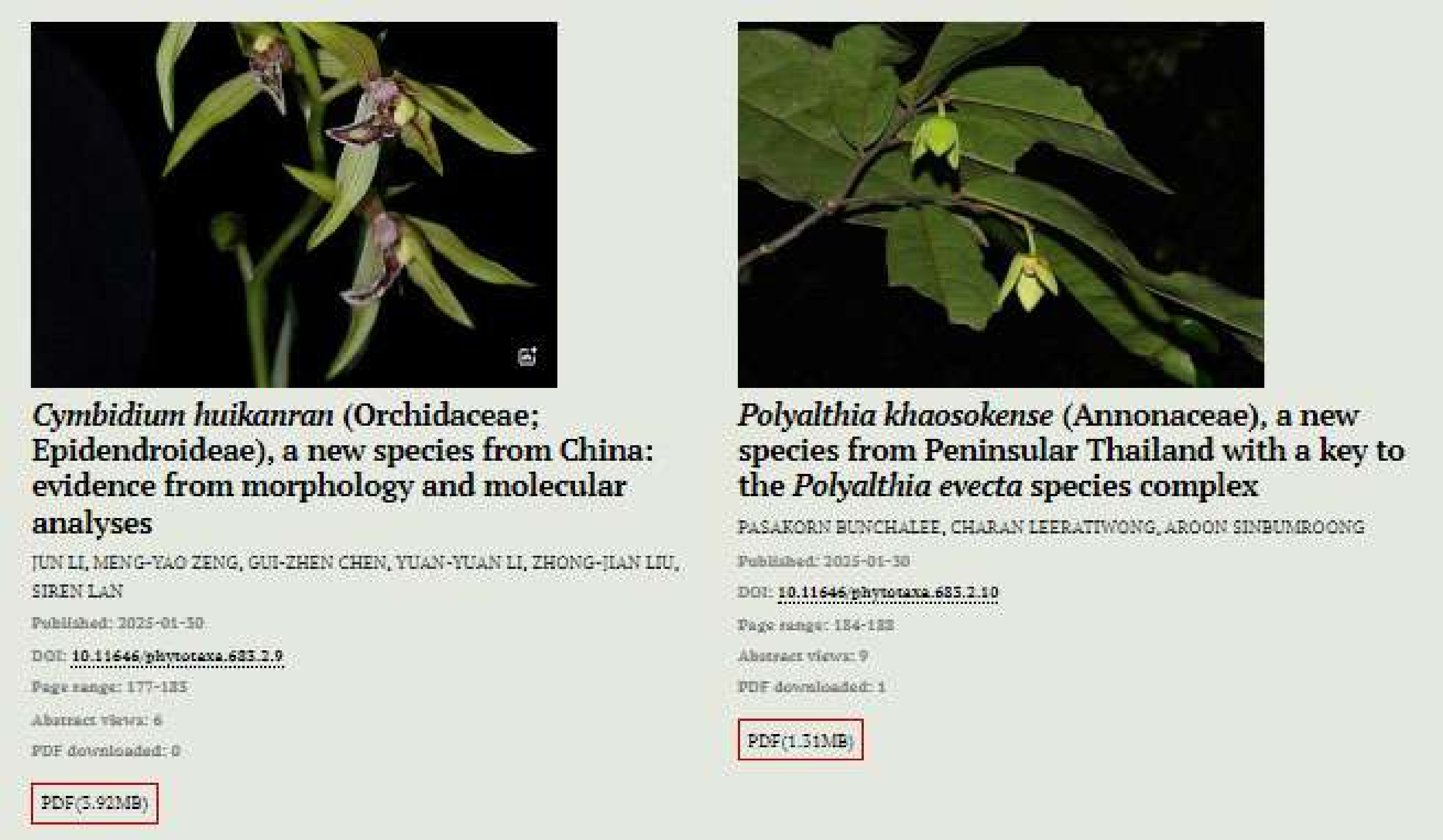

Cymbidium huikanran (Orchidaceae; Epidendroideae), a new species from China: evidence from morphology and molecular analyses

JUN LI, MENG-YAO ZENG, GUI-ZHEN CHEN, YUAN-YUAN LI, ZHONG-JIAN LIU, SIREN LAN

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Polyalthia khaosokense (Annonaceae), a new species from Peninsular Thailand with a key to the *Polyalthia evecta* species complex

PASAKORN BUNCHALEE, CHARAN LEERATIWONG, AROON SINBUMROONG

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Molecular phylogeny and morphology reveal a new wood-inhabiting fungus, *Hyphoderma cinereofuscum* (Polyporales, Basidiomycota), from southwest China

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Abstract

Hyphoderma is one of the important representative groups of wood-inhabiting fungi. These fungi secrete various enzymes capable of degrading cellulose, hemicellulose, and lignin into simple inorganic substances. The taxa within the genus cause a white rot of wood, play a key role in the carbon cycle and are the most efficient wood decomposers in the forest ecosystem. This study proposes a new wood-inhabiting fungal taxon, *Hyphoderma cinereofuscum*, based on morphological features and molecular evidence. It is characterized by the white hymenial surface, a monomitic hyphal system, generative hyphae with simple-septa, colorless, thin-walled, the presence of the tubular and capitate cystidia, and cylindrical basidiospores 9–11.5 × 4.5–5 µm. The phylogenetic tree inferred from a combination of the internal transcribed spacer regions (ITS) and the large subunit nuclear ribosomal RNA gene (nLSU) revealed that *Hyphoderma cinereofuscum* nested in the *Hyphoderma* clade and is closely related to *H. marginatum*. A full description, illustrations and phylogenetic analysis results of the new species are provided.

Key words: Biodiversity, Classification, New taxon, Phylogenetic analysis, Taxonomy, Wood-decaying fungi

Introduction

Fungi play fundamental ecological roles as decomposers, pathogens, and mutualists of plants and animals (Tedersoo *et al.* 2014, James *et al.* 2020, Hyde *et al.* 2023, Yuan *et al.* 2023). In forest ecosystems, fungi drive carbon cycling in forest soils, mediate the mineral nutrition of plants, and alleviate carbon limitations (Wei & Dai 2004, Tedersoo *et al.* 2014, Rokas *et al.* 2018, James *et al.* 2020).

Wood-inhabiting fungi are a cosmopolitan group that has a rich diversity in boreal, temperate, subtropical, and tropical regions (Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014, Dai *et al.* 2015, 2021, Wu *et al.* 2020, 2022a, Luo *et al.* 2022, Duan *et al.* 2023, Yang *et al.* 2024, Zhao *et al.* 2023, 2024). Many new taxa from the family Hyphodermataceae are reported recently (Yurchenko & Wu 2015, Luo *et al.* 2022, Wijayawardene *et al.* 2022, Yang *et al.* 2023, Dong *et al.* 2024).

The genus *Hyphoderma* Wallr. (1833: 576) (Hyphodermataceae, Polyporales) represents one of the richest species and taxonomically complicated genera among wood-inhabiting fungi, typified by *H. setigerum* (Fr.) Donk. (1957: 15) (Donk 1957, Kirk *et al.* 2008, Yurchenko & Wu 2015). The species of *Hyphoderma* cause white rot (Wu 1997) (Floudas *et al.* 2012, Duan *et al.* 2023). *Hyphoderma* is characterized by the resupinate to effuse-reflexed basidiomata with ceraceous consistency, smooth to tuberculate or hydnoid hymenophore, a monomitic hyphal structure (rarely dimitic) with clamp connections on generative hyphae, cystidia or not, basidia suburniform to subcylindrical and cylindrical, smooth, thin-walled, ellipsoid to subglobose basidiospores (Wallroth 1833, Bernicchia & Gorjón 2010).

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A total of, 211 specific and infraspecific names are recorded in Index Fungorum (http://www.indexfungorum.org; accessed on 7 January 2025) and MycoBank (https://www.mycobank.org). Currently, 117 species have been accepted worldwide (Donk 1957, Nakasone 2008, Wu *et al.* 2010, Baltazar *et al.* 2016, Martín *et al.* 2018, Guan & Zhao 2021a, Ma *et al.* 2021, Duan *et al.* 2023, Yang & Zhao 2023, Su *et al.* 2023).

Molecular systematics, including *Hyphoderma* based on the internal transcribed spacer (ITS), revealed the classification of corticioid fungi, which showed that *H. obtusum* J. Erikss. (1958: 16) and *H. setigerum* clustered into the family Meruliaceae Rea, and the large subunit nuclear ribosomal RNA gene (nLSU) regions, revealed the classification of corticioid fungi, which showed that *H. obtusum* J. Erikss. (1958: 16) and *H. setigerum* clustered into the family Meruliaceae Rea, and then grouped with the taxon *Hypochnicium polonense* (Bres.) Donk (1957: 15) (Larsson 2007). Tellería *et al.* (2012) discussed the relationships between *Hyphoderma* and *Peniophorella* P. Karst.1889, in which some species from both genera were grouped and proposed a new species, *H. macaronesicum* Tellería, *et al.* (2012: 1125). The research focusing on the *H. setigerum* complex showed that *H. pinicola* Yurchenko & Sheng H. Wu (2014: 2) represented the fifth species in this complex, and the result revealed that this complex occurred worldwide from tropical to temperate regions (Yurchenko & Wu 2014a, b). A revised family-level classification of the order Polyporales revealed that four species of *Hyphoderma* nested into the residual polyporoid clade, belonging to the family Hyphodermataceae, and they were grouped with three related genera *Meripilus* P. Karst.1882, *Physisporinus* 1889 P. Karst. and *Rigidoporus* Murrill (Justo *et al.* 2017). The research was carried out based on morphology and phylogeny, in which two new species, *H. fissuratum* C.L. Zhao & X. Ma (2021: 37) and *H. mopanshanense* C.L. Zhao (2021: 39), were proposed, and the genus species of *Hyphoderma* were compared with closely related taxa (Ma *et al.* 2021).

During the surveys of wood-inhabiting fungi, we discovered a species of *Hyphoderma* in Yunnan Province, China, which was inconsistent with any known species of wood-inhabiting fungi. We carried out a phylogenetic and taxonomic study on *Hyphoderma* based on the ITS+nLSU sequences to clarify the species' placement and relationships.

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata of fungi growing on angiosperm branches were collected from Tongbiguan Provincial Nature Reserve, Yingjiang County, Dehong, Yunnan Province, China. The samples were photographed in situ, and important collection information (Rathnayaka *et al*. 2024) and fresh macroscopic details were recorded (Dong *et al*. 2024). All photos were stacked and merged using Helicon Focus Pro 7.7.5 software. Specimens were dried in an electric food dehydrator at 40 °C (Dong *et al.* 2022, Hu *et al.* 2022), and then sealed and stored in an envelope bag and deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China.

Morphology

Macromorphological descriptions were based on field notes and photos captured in the field and lab. Color terminology followed Petersen (1996). Micromorphological data were obtained from the dried specimens following observation under a light microscope (Zhao *et al.* 2023, Dong *et al*. 2024). The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB = cotton clue, CB– = acyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied and n = a/b (number of spores (a) measured from a given number (b) of specimens). Q_m represented the average Q of basidiospores measured ± standard deviation.

DNA extraction

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, P.R. China) was used to obtain genomic DNA from the dried specimens. The nuclear ribosomal ITS region was amplified with primers ITS5 and ITS4 (White *et al.* 1990). The nuclear nLSU region was amplified with primer pair LR0R and LR7 (Vilgalys & Hester 1990).

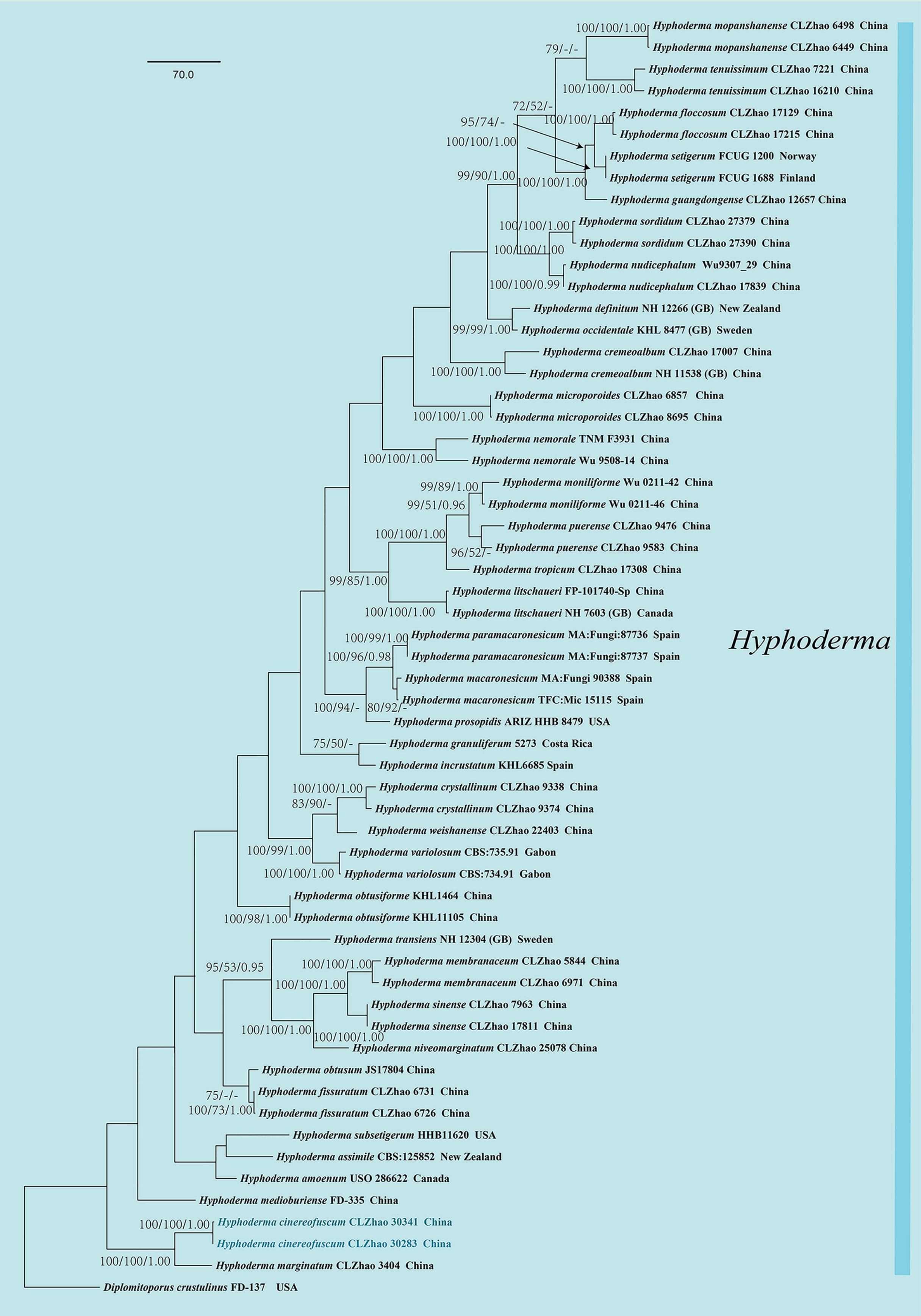

FIGURE 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Hyphoderma* based on the concatenated ITS+nLSU dataset. The branch is labeled with the Maximum Likelihood bootstrap values equal to or higher than 70 %, Maximum Parsimony bootstrap values equal to or greater than 50%, and the Bayesian Posterior Probability equal to or greater than 95%. The new species is bold.

PCR amplification, sequencing

The PCR procedure for ITS was as follows: initial denaturation at 95°C for 3 min, followed by 35 cycles at 94°C for 40 s, 58°C for 45 s, and 72°C for 1 min, and a final extension of 72°C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94°C for 1 min, followed by 35 cycles at 94°C for 30 s, 48°C for 1 min, and 72°C for 1.5 min, and a final extension of 72°C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). All newly generated sequences were deposited in NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank/). These sequences, along with sequences from closely related taxa, are given in Table 1.

TABLE 1. Names, voucher numbers, countries, references, and corresponding GenBank accession numbers of the taxa used in this study. The new species is in bold.

Species Name	**Sample No.**	**GenBank Accession No.**		**References**	**Country**
		ITS	**nLSU**		
Diplomitoporus crustulinus	FD-137	KP135299	KP135211	Justo *et al*. 2017	USA
Hyphoderma amoenum	USO 286622	HE577030		Telleria *et a*l. 2012	Canada
H. assimile	CBS:125852	MH863808	MH875272	Vu *et al*. 2019	New Zealand
H. cinereofuscum	**CLZhao 30341**	**PQ492371**	**PQ511128**	**Present study**	**China**
H. cinereofuscum	**CLZhao 30283**	**PQ492372**	**PQ511129**	**Present study**	**China**
H. cremeoalbum	NH 11538 (GB)	DQ677492	DQ677492	Larsson 2007	China
H. cremeoalbum	CLZhao 17007	OM985716	OM985753	Duan *et al*. 2023	China
H. crystallinum	CLZhao 9338	MW917161	MW913414	Guan & Zhao 2021	China
H. crystallinum	CLZhao 9374	MW917162	MW913415	Guan & Zhao 2021	New Zealand
H. definitum	NH 12266 (GB)	DQ677493	DQ677493	Larsson 2007	China
H. fissuratum	CLZhao 6731	MT791331		Ma *et al*. 2021	China
H. fissuratum	CLZhao 6726	MT791330	MT791334	Ma *et al*. 2021	China
H. floccosum	CLZhao 17129	MW301683	MW293733	Guan & Zhao 2021b	China
H. floccosum	CLZhao 17215	MW301687	MW293735	Guan & Zhao 2021b	Costa Rica
H. granuliferum	5273	JN710545	JN710545	Yurchenko & Wu 2014	Canada
H. guangdongense	CLZhao 12657	PP235513	PP235514	Su *et al*. 2024	China
H. incrustatum	KHL6685		AY586668	Yurchenko & Wu 2014	Spain
H. litschaueri	NH 7603 (GB)	DQ677496	DQ677496	Larsson 2007	Spain
H. litschaueri	FP-101740-Sp	KP135295	KP135219	Duan *et al*. 2023	China
H. macaronesicum	MA:Fungi 90388	KC984327		Telleria *et al*. 2018	USA
H. macaronesicum	TFC:Mic 15115	HE577011		Yurchenko & Wu 2014	China
H. marginatum	CLZhao 3404	OM985717	OM985754	Duan *et al*. 2023	China
H. medioburiense	FD-335	KP135298	KP135220	Floudas & Hibbett 2015	China
H. membranaceum	CLZhao 5844	MW917167	MW913420	Guan & Zhao 2021	China
H. membranaceum	CLZhao 6971	MW917168	MW913421	Guan & Zhao 2021	China
H. microporoides	CLZhao 6857	MW917169	MW913422	Guan & Zhao 2021	China
H. microporoides	CLZhao 8695	MW917170	MW913423	Guan & Zhao 2021	China
H. moniliforme	Wu 0211-42	KC928282		Yurchenko & Wu 2015	China
H. moniliforme	Wu 0211-46	KC928284		Yurchenko & Wu 2015	China
H. mopanshanense	CLZhao 6498	MT791329	MT791333	Ma *et al*. 2021	China

......continued on the next page

TABLE 1. (Continued)

Species Name	Sample No.	GenBank Accession No.		References	Country
		ITS	nLSU		
H. mopanshanense	CLZhao 6449	OM985720	OM985759	Duan *et a*l. 2023	China
H. nemorale	TNM F3931	KJ885183	KJ885184	Yurchenko & Wu 2015	China
H. nemorale	Wu 9508-14	KC928280	KC928281	Yurchenko & Wu 2015	China
H. niveomarginatum	CLZhao 25078	OR141728	OR506179	Yang *et al.* 2023	China
H. nudicephalum	Wu9307_29	AJ534269		Nilsson *et al.* 2003	China
H. nudicephalum	CLZhao 17839	OM985721	OM985760	Duan *et al.* 2023	Sweden
H. obtusiforme	KHL1464	JN572909		Yurchenko & Wu 2014	Spain
H. obtusiforme	KHL11105	JN572910		Yurchenko & Wu 2014	Spain
H. obtusum	JS17804		AY586670	Yurchenko & Wu 2014	China
H. occidentale	KHL 8477 (GB)	DQ677499	DQ677499	Larsson 2007	China
H. paramacaronesicum	MA:Fungi 87736	KC984399		Martín *et al.* 2018	USA
H. paramacaronesicum	MA:Fungi 87737	KC984405		Martín *et al.* 2018	China
H. prosopidis	ARIZ HHB 8479	HE577029		Yurchenko & Wu 2015	China
H. puerense	CLZhao 9476	MW443045		Guan *et al.* 2021	Norway
H. puerense	CLZhao 9583	MW443046	MW443051	Guan *et al.* 2021	Finland
H. setigerum	FCUG 1200	AJ534273		Nilsson *et al.* 2003	China
H. setigerum	FCUG 1688	AJ534272		Nilsson *et al.* 2003	China
H. sinense	CLZhao 7963	MW301679	MW293730	Guan & Zhao 2021b	China
H. sinense	CLZhao 17811	MW301682	MW293732	Guan & Zhao 2021b	China
H. sordidum	CLZhao 27379	OR141731		Yang *et al.* 2023	USA
H. sordidum	CLZhao 27390	OR141732	OR506180	Yang *et al.* 2023	China
H. subsetigerum	HHB11620	GQ409521		Yurchenko & Wu 2014	China
H. tenuissimum	CLZhao 7221	MW443049	MW443054	Guan *et al.* 2021	Sweden
H. tenuissimum	CLZhao 16210	MW443050	MW443055	Guan *et al.* 2021	China
H. transiens	NH 12304 (GB)	DQ677504	DQ677504	Larsson 2007	Gabon
H. tropicum	CLZhao 17308	OM985727	OM985768	Duan *et al.* 2023	Gabon
H. variolosum	CBS:734.91	MH862320	MH873992	Vu *et al.* 2019	China
H. variolosum	CBS:735.91	MH862321	MH873993	Vu *et al.* 2019	China
H. weishanense	CLZhao 22403	OR141727	OR506181	Yang *et al.* 2023	China

Phylogenetic analyses

The sequences were aligned in MAFFT version 7 (Katoh *et al.* 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was aligned first and then ITS sequences were combined with Mesquite version 3.51. *Diplomitoporus crustulinus* (Bres.) Domanski (1970: 192) was selected as an outgroup taxon for the phylogenetic analyses of the ITS following a previous study (Justo *et al.* 2017). Maximum Parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined three datasets. Approaches to phylogenetic analyses followed Zhao & Wu (2017). MP analysis was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Maxtrees were set to 5000, branches of zero length were collapsed, and all most parsimonious trees were saved.

Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), the consistency index (CI), the retention index (RI), the rescaled consistency index (RC), and the homoplasy index (HI) were calculated for each most-parsimonious tree generated. ML was inferred using RAxML-HPC2 through the CIPRES Science Gateway (www.phylo.org) (Miller *et al.* 2012). Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates and evaluated under the gamma model.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian Inference (BI), which was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist *et al.* 2012). A total of 4 Markov chains were run for 2 runs from random starting trees for four million generations for ITS+nLSU (Fig. 1), with trees and parameters sampled every 1000 generations. The first one-fourth of all generations were discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received Maximum Likelihood bootstrap value (BS) ≥ 70%, Maximum Parsimony bootstrap value (BT) ≥ 50%, or Bayesian posterior probabilities (BPP) ≥ 0.95.

Results

Phylogenetic analyses

The dataset based on ITS+nLSU comprises sequences from 59 fungal specimens representing 39 species. The dataset had an aligned length of 2868 characters, of which 1416 characters are constant, 118 are variable and parsimony-uninformative, and 502 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 2868, CI = 0.3508, HI = 0.6492, RI = 0.6448 and RC = 0.2262). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.010233 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 1075.5.

The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences revealed that *Hyphoderma cinereofuscum* grouped into the genus *Hyphoderma*, in which it closely grouped with the taxon *H. marginatum* Z.Y. Duan & C.L. Zhao (2023: 7).

Taxonomy

Hyphoderma cinereofuscum W. Li & C.L. Zhao, *sp. nov.* Figs. 2, 3
MycoBank no.: MB 856300

Etymology—*Cinereofuscum* (Lat.) refers to the species having fuscous basidiomata with cinereous hymenial surface.

***Holotype*:**—CHINA. Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 24°35' N, 97°39' E, altitude 1006 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 19 July 2023, CLZhao 30341 (SWFC).

***Basidiomata*:**—Annual, resupinate, adnate, coriaceous, odorless when fresh, up to 26 cm long, 3.5 cm wide, and 50–100 µm thick. Hymenial surface smooth, white to cream when fresh, and cinereous and fuscous when dry. Sterile margin cinereous, up to 2 mm wide.

***Hyphal system*:**—Monomitic; generative hyphae with simple-septa, colorless, thin-walled, branched, interwoven, 2.5–3.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

***Hymenium*:**—Cystidia of two types: 1) tubular cystidia, colorless, thin-walled, 25.9–37.1 × 1.8–2.5 µm; 2) capitate cystidia, colorless, thin-walled, 12.5–15.5 × 6.2–7 µm. Basidia clavate to subcylindrical, more or less constricted in the middle, with four sterigmata and a basal simple septum, 23.5–26 × 5.3–6.5 µm; basidioles dominant, similar to basidia in shape, but slightly smaller, and usually with a few guttules.

***Spores*:**—Basidiospores cylindrical, colorless, thin-walled, smooth, and usually with a few guttules, IKI–, CB–, (8.5–)9–11.5(–12) × (4–)4.5–5(–5.5) µm, L = 10.04 µm, W = 4.59 µm, Q = 2.17–2.22, Q_m = 2.19 ± 0.15 (n = 60/2).

***Additional specimen examined* (*paratype*):**—CHINA. Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 24°35' N, 97°39' E, altitude 1006 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 19 July 2023, CLZhao 30283 (SWFC).

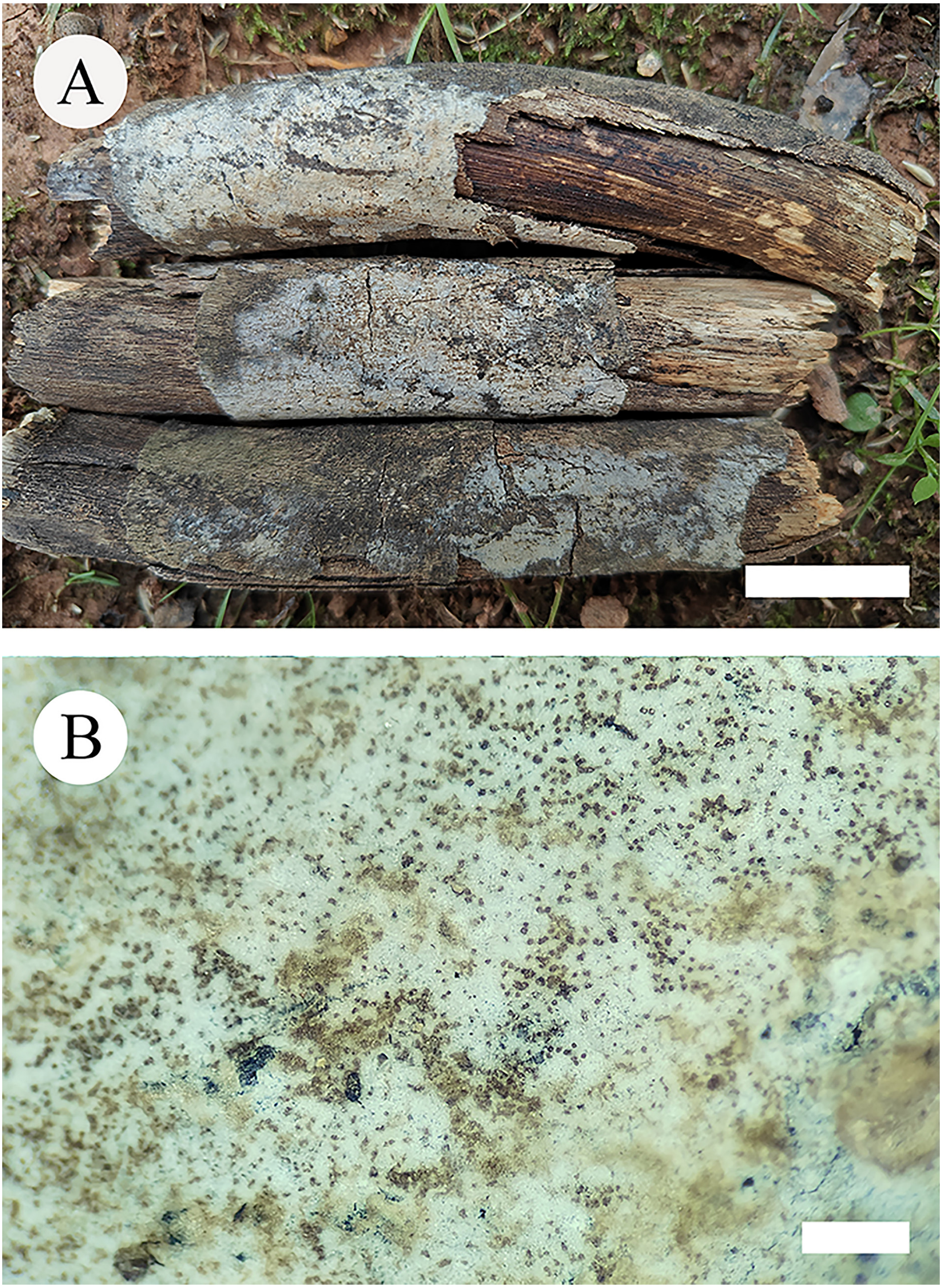

FIGURE 2. *Hyphoderma cinereofuscum* (holotype, CLZhao 30341): basidiomata on the substrate (A), macroscopic characteristics of hymenophore (B). Bars: (A) = 2 cm and (B) = 1 mm.

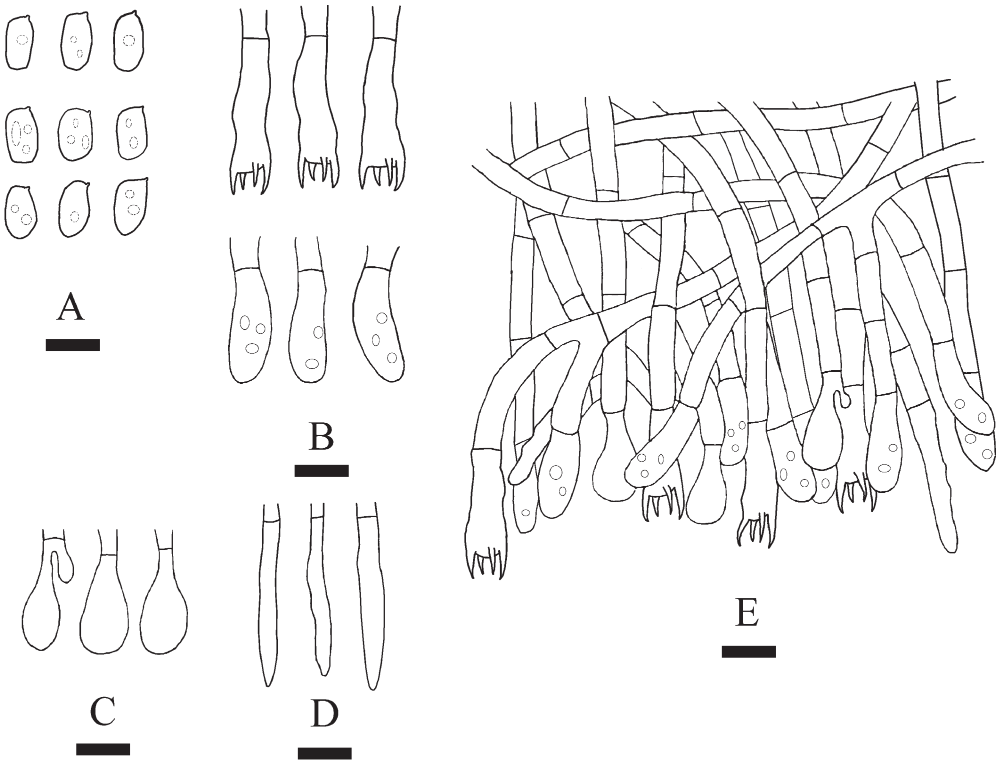

FIGURE 3. Microscopic structures of *Hyphoderma cinereofuscum* (holotype, CLZhao 30341): basidiospores (A), basidia and basidioles (B), capitate cystidia (C), tubular cystidia (D), a section of the hymenium (E). Bars: (A–E) = 10 µm.

Discussion

The family-level classification research of Polyporales (Basidiomycota) based on nLSU, ITS, and RPBl genes revealed that four species *Hyphoderma macaronesicum*, *H. medioburiense* (Burt) Donk (1957: 15), *H. mutatum* (Peck) Donk (1957: 15), and *H. setigerum* were nested in the family Hyphodermataceae within the residual polyporoid clade (Justo *et al.* 2017). In this study, the phylogenetic tree (Fig. 1) inferred from the ITS+nLSU gene regions revealed that *Hyphoderma cinereofuscum sp. nov.* is closely related to the taxon *H. marginatum*. However, *H. marginatum* differs from *H. cinereofuscum* by having a cream hymenial surface and narrower basidiospores (9–10 × 3.5–4.5 µm vs. 9–11.5 × 4.5–5 µm, Duan *et al.* 2023).

Morphologically, *H. cinereofuscum* is similar to *H. niveomarginatum* Yang Yang & C.L. Zhao (2023: 9) and *H. tenuissimum* C.L. Zhao & Q.X. Guan (2021: 83) by having the cylindrical basidiospores. However, *H. niveomarginatum* is distinguished from *H. cinereofuscum* by its yellowish hymenial surface and clamped generative hyphae (Yang & Zhao 2023). *Hyphoderma tenuissimum* differs from *H. cinereofuscum* by its tuberculate to minutely-grandinioid hymenial surface, and narrower basidiospores (7–10.5 × 3–4.5 µm, vs 9–11.5 × 4.5–5 µm, Guan & Zhao 2021a).

Wood-inhabiting fungi are generally found in dead tree trunks, inverted wood, and artificial wood products, and they play a pivotal role in forest ecosystems as decomposers (Dai 2011, Tedersoo *et al.* 2014, Cui *et al.* 2019, James *et al.* 2020, Wu *et al.* 2020, 2022b, Dai *et al.* 2021, Luo & Zhao 2023, Liu *et al.* 2023, Hussain *et al.* 2024). Based on the morphological and phylogenetic methods, many wood-inhabiting fungi were recorded in China (Wu *et al.* 2019, 2020, 2022b, Dai *et al.* 2021, Wang *et al.* 2021, Luo & Zhao 2022, Ji *et al.* 2022, Mao *et al.* 2023, Zhang *et al.* 2023, Zhao *et al.* 2023, 2024, Dong *et al.* 2024). The genus *Hyphoderma*, a crucial representative group of wood-inhabiting fungi (Bernicchia & Gorjón 2010), currently boasts 38 species in China (Guan & Zhao 2021a, b, Guan *et al.* 2021, Ma & Zhao 2021, Zong *et al.* 2021, Gu & Zhao 2022, Deng & Zhao 2023, Duan *et al.* 2023, Yang *et al.* 2024). However, the urgency for further fieldwork and molecular analyses to enrich the species diversity of this genus cannot be overstated.

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